Manual

LightningCeph

Version 1.0.0





ElleSoft srl LightningCeph

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23rd January 2001

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1.0 Introduction

Lightning Ceph is a software application specifically designed to perform cephalometric analyses, the clinical treatment of patient orthodontic problems, Bolton analysis, the analysis of anterior discrepancy and spatial analysis, all quickly and easily and constantly prompted.

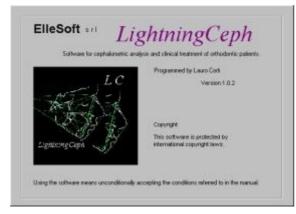
LightningCeph translates each individual value recorded into its corresponding clinical meaning, it integrates the landmark points entered, and in relation to the age and sex of the patient concerned, generates a detailed diagnostic evaluation, and also permits tracings to be superimposed in any format required.

LightningCeph allows you to conduct cephalometric analyses directly from scanned x-rays saved to disk. If you don't have access to a scanner, or if you need an extra-quick analysis, LightningCeph lets you use the screen like a negatoscope, and also lets you conduct customised cephalometric analyses.

The need to use a digitizer has been eliminated.

With LC, you don't have to be an expert in cephalometrics, because the programme will automatically guide you step-by-step as to the points to click, and generates a written summary description and a graphical example. When the guided process to locate the individual landmarks has been completed, the programme generates a detailed and surprisingly accurate diagnostic report.

2.0 Warranty and Rights of Use



Using LightningCeph means implicitly accepting each of the conditions detailed below.

The programme is protected by stringent copyright law, and is the property of its owner who may licence it to users who will then be entitled to use it on only one personal computer. The programme must not be given in use to other professionals in any form whatsoever. Users are entitled to a replacement if the magnetic disk should be damaged, for requests received within 30 days from the date of receipt.

Programme codes must not be edited.

The protection dongle will be replaced only if it can be proved that the damage was not provoked by the user.

For all other matters, the programme is supplied with no further form of warranty.

The programme is intended for use by doctors under their full liability, and only after having first evaluated the programme's featured characteristics and limits; the manufacturer will not be held liable for any type of damage caused by eventual malfunctioning of the programme.

3.0 Configuration

The minimum system setup requirements are: Pentium with 32 MB RAM.

The programme will process with exceptional speed when 500 MH processors with 64MB RAM or above are used.

To optimise image display, a 17" monitor with good quality video card are advised.

Set the screen resolution to 800 x 600 pixels and 65,536 colours.

4.0 Installation

Remove the demo version if need be, by eliminating the directory: C:\Lightning Ceph.

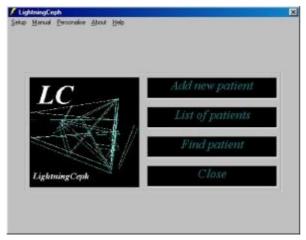
Insert the CD and double click Setup, following the instructions that will appear on the screen, clicking yes to install C:\LightningCeph.

NB: the manual has been purposely compiled to be concise; the manufacturer advises that after having read the manual through, users familiarise themselves with the application using the tool tip text (position the mouse pointer over the button that you want to receive information

on) and study the "?" menu commands that provide handy hints as to the various parts of the programme.

Clearly, the manufacturer reserves the right to edit or modify the programme without prior notice.

5.0 Starting up the programme

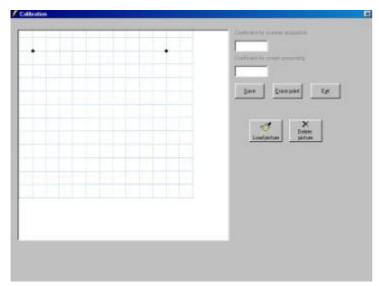


Once the protection dongle had been fitted to the PC parallel port and the correct driver loaded (Hldrv32.exe), run Windows, set the screen resolution to 800 x 600 pixels, click Start C > LightningCeph, and the window shown here will be displayed (Menu).

NB: since the code has been encrypted, when the programme is run it will take a few seconds for decodification to be completed.

Menu

6.0 System calibration and Setup



The system must be calibrated in order to perform correctly. To do this, from the menu click Setup > Calibration: the window illustrated will appear. By means of the " Load picture " button, load a previously scanned image, saved in a directory according to your system organisation, with two points ten centimetres apart, use this to replace the example, follow the instructions, save and exit. The angles and relationships will always be correct. However, the distances will be the same as the real ones. AND **CONSEQUENTLY ALSO THE** DIAGNOSTIC REPORT, only when the

If the calibration configuration is modified following modifications to the operating system (for example, if you decide to scan with a different resolution from the one currently preset), this will affect the linear values of all previously elaborated images.

It is advisable to carry out some trials first in order to adapt results to the hardware currently being used, in order to set up an operating standard that will not require any further modification.

The bitmap images in the programme files refer to x-rays scanned at 75 dpi. The above programme default coefficients regard images imported from a scanner, and a 17" monitor for screen processed images.

This means that if a 75 dpi resolution image is used when scanning images for later acquisition, or if the image to be used is imported directly from a 17" monitor screen, the system doesn't have to be calibrated.

If the image captured at 75 dpi (recommended resolution) is satisfactory, and the screen being used is not a 17" one, when calibrating the system for the first two points, use the default image, whereas for the second two points, place a ruler above the screen and click at a distance of 10cm.

Given that even when a 17" monitor is used, minute differences can be found depending on the particular regulation that is set when the monitor is being adjusted, it is advisable to carry out the calibration to further ensure system accuracy.

To make these procedures as simple as possible:

always use 75 dpi to capture bitmap images and carry out system calibration as per the instructions using the previously loaded image.

7.0 Heading Line



To set headings with the name of the owner's surgery: from the Menu, click Setup > Heading; when the window illustrated here opens, complete the text boxes and choose the desired colour from the Font Colour menu.

8.0 Image Acquisition

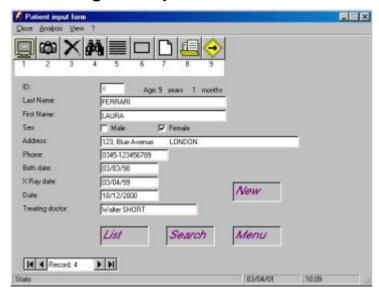
The images to be elaborated must be captured beforehand with a scanner and saved in a

directory created specifically for the purpose. The name given to an image must not exceed 50 characters (including spaces path and extension), given that longer names could provoke errors.

Alternatively, images can be manipulated by superimposing the x-ray on the screen that would then act as a negatoscope.

It will be widely found that the best solution will be to capture an 18-20 cm square on the x-ray with the scanner set at a resolution of 75 dpi, then save the images as bitmaps or JPG's. It is advisable to carry out some trials first in order to adapt results to the hardware currently being used, in order to set up an operating standard that will not require any further modification.

9.0 Adding a new patient



From the menu window, click "Add new patient" or from the patient input form window (see picture for example), click "New" or click button 7.

When the patient input form appears to enable you to insert a new patient's data, the following five fields must be completed: Name, Surname, Sex, Date of Birth, X-ray date. Double clicking inside any text box will display the data of the associated feature.

Patient Input Form

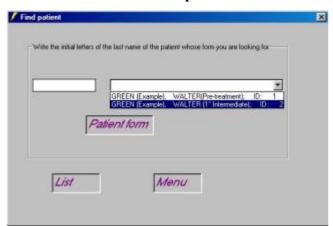
It will be impossible to move to any other window if these obligatory fields have not been filled out, therefore it is advisable to click "*New*" or similar command only when these data do actually have to be inserted.

10.0 Deleting a patient input form

To cancel a patient input form, click button 3 on the patient input form.

If you click "New", the cancel function will be disabled until the programme is restarted.

11.0 Find a Patient Input Form



From the Menu window, or from the equivalent patient input form command, click " Find patient", when the window shown to the left appears, type the initial letters of the required patient's surname in the text box, scroll down with the arrow that appears as soon as you key in these letters, select the name that you require and click "patient form".

Find a patient

Alternatively, to call up a patient input form, you can double click the ID number in the list window (example shown).

To change the background colour of the list window, click or double click the LC icon.

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363	CLAMMACHELLA	MARKO	10/05/90	23/08/00	Menu
527	COMMOCHELLA	LURENCO	10/10/99	28/09/00	
300	CLAHMACHELLA	LORENCE	10/10/09	15/10/00	
546	CLEMBERCHELLA	GUGLELMO	28/11/90	00/09/00	
364	CLAHMINCHELLA MISPICE	FREM SCREEN	02/02/98	23/09/00	
406	GCCH86	DAVICE	05/06/66	25/04/58	
312	OMNI	CLAUDIA.	16/09/90	17/09/98	
500	CORULLA .	PRIMACE/SCO	25/00/00	02/10/00	
	ORELLA	FRANCESCO	25/08/00	20/11/06	
	DOCODCIA.	SERENA	06/04/99	07/11/00	
	COMMENTUCO	MORE	07/01/89	06/11/98	
	CORFI	G08	03/03/90	11/09/98	
	CHEMONETE	MEREA	25/10/99	12/11/99	
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367	B ERAMO	44.64	07/03/90	25/06/97	100
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	01 MC000	ALBERTO:	13/05/61	22/01/01	
211	DINICOLA	MARIA PIA	29/06/7E	19/03/98	
124	DI POMPED	RIGHTING	06/01/90	19/09/00	-1

12.0 Case history / record examination

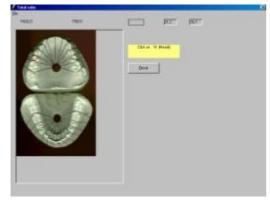


The patient's case history can be opened from the patient input form by clicking on the menu bar, View > Case history or by pressing button 6. The same commands can also be found in other windows.

Although the case history is particularly indepth, overall, it is easy to understand and use.

More detailed information is provided later.

12.1 Bolton Analysis



Before running the Bolton Analysis function, a plaster model image must be captured from the scanner and saved in a directory created specifically for the purpose. The name given to an image must not exceed 50 characters (including spaces path and extension), given that longer names could provoke errors. Click the "Calculate Bolton index" then follow the instructions as indicated in the window shown here.

NB: LC performs extremely accurate Bolton analysis, although you must first carefully locate the mesial and distal points for each dental feature otherwise the results will not be particularly reliable. You may find it useful to draw on the points, or better still, draw a black thread between the interdental spaces.

12.2 Anterior discrepancy

The procedure used to calculate anterior discrepancy is similar to the previous one.

12.3 Spatial analysis

The programme does the spatial analysis automatically once the full Bolton Analysis has been performed.

12.4 Image Database

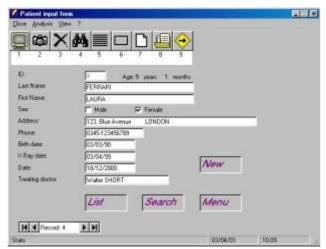
The tracing background and plaster models are loaded automatically in the image database section of the case history when you reply positively to the questions presented when the Bolton analysis, anterior discrepancy calculation, superimpose function or tracings on free backgrounds are started up. Other images can be loaded be clicking the "Load picture" button, as and when may be required.

To delete an image, click the Delete button.

12.5 Diary

This page is reserved for the day-to-day notes on treatment carried out. When you insert the secret code, which you'll receive separately, in the bottom right text box another text box will be displayed (otherwise it remains hidden) where confidential data can be inserted if necessary. By clicking OK again the box will go away and remain invisible until called up again.

13.0 Cephalometric Analysis

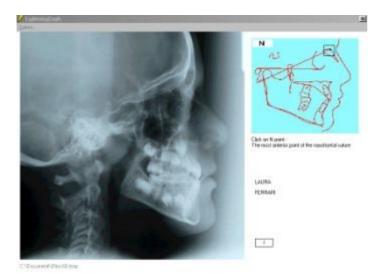


Patient input form: to read the functions of each of the tool bar buttons, position the mouse pointer over the button concerned (Tool tip text).

When the form has been completed (example shown), double-click button 2 (camera) to load up the image to the LC database from the directory where it was previously saved: search and select the image.

If you would rather use the screen as a negatoscope, click button 1 (screen), the window illustrated to the right will then open automatically (Select methodology), select your preferred option and click OK. (The default method is the Comparative analysis).





At this stage, the window shown below will be displayed (locating landmarks).

If you previously selected the screen image processing option, instead of the x-ray, window shown to the left will be displayed with a plain, white background which the x-ray to be examined must be physically superimposed on; the various points to be located on the image are indicated and explained in a table at the top right of this window. If the image should disappear, click where it was and it will be displayed again.

If a landmark is incorrectly drawn or if you wish to delete all points drawn, use the tool bar and pop up menu commands (right mouse button).

When a single point is deleted, it will turn white.

Special Feature: when the pull-down menu is opened, the points drawn on the screen where the pull down part is shown will be physically cancelled from the screen (but not from the memory).



When all landmark points have been located, the window shown opposite will appear that amongst other things, allows you to select your preferred tracing colour, otherwise blue will be the default colour.

Click inside the picture box to display the results of the analysis, the next screen will be the one shown here (tracing) that allows various options to be performed.

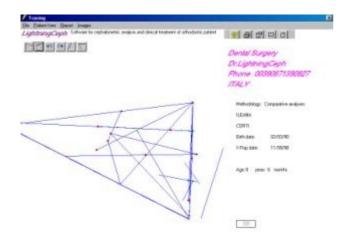
To read the functions of each of the tool bar buttons, position the mouse pointer over the button concerned (Tool tip text).



Tracing

The tracing window menus are clear and require no explanation, whilst the image menu merits a closer look:

13.1 Tracings on a white background



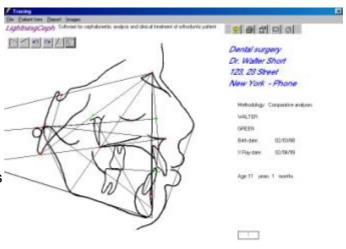
It functions rather like the last button from the right on the toolbar, and lets you view the "plain tracing" on a white background.

To freely move the tracing around, use the buttons located at the top left of the window.

13.2 Tracings on free background

This function allows you to position the tracing on any background whatsoever, previously scanned and saved in the usual image directory.

If you need to combine the tracing with the patient's profile and main anatomical structures, using your negatoscope and traditional tracing paper, you should simply and easily draw what you require, once this drawing has been scanned and uploaded (to superimpose it on a white background you'll need to cover the tracing paper with another sheet of white paper), it can then be used as the basis for a tracing.



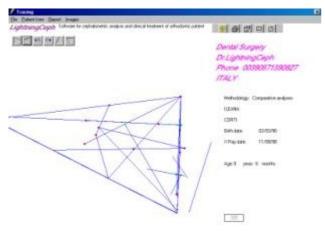
Alternatively, the tracing can be done on any other kind of previously uploaded background, whether it be a coloured base, a logo, or any other kind of image that you may require.

To freely move the tracing around, use the buttons located at the top left of the window.

13.3 Tracings on an X-ray

This function displays the tracing on a scanned x-ray or on a white background if the acquisition was not done using a scanner (tracing window).

13.4 Superimpose on a white background



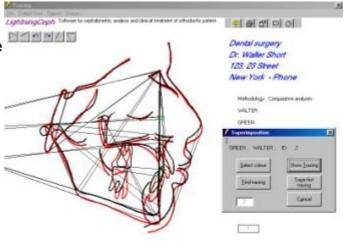
When you click this menu, the "Superimpose" window appears (compared with the image shown below, in this case only a white background is shown, rather than the anatomical profile drawing), from which you can immediately do the first tracing from the currently selected record. To change the first tracing or to choose the next one, use the "Find tracing" button and a window not unlike the "find patient" one will open, as regards its features and functions. The tracing colour can be defined with the "Select colour" button. Once the first tracing is in position and saved using the "Save first tracing" button,

find and select the second tracing, click the "Show tracing" button again then double-click with the right button of the mouse to position the second tracing too. To freely move the tracings around and to superimpose images on any plane, use the buttons located at the top left of the window. The resulting image is shown above.

13.5 Superimposing images

To superimpose tracings on anatomic profiles, the sheets of tracing paper with the previously completed drawings must be superimposed and covered with a sheet of white paper then scanned. The resulting image can then be used as the basis for future superimposed images.

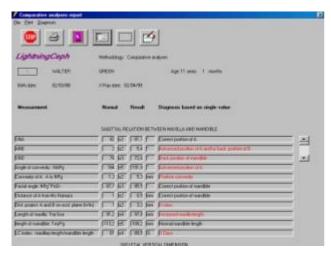
When you click this menu, window 6 appears, from which you can immediately do the first tracing from the currently selected record. To change the first tracing or to choose the next one, use the "Find tracing" button and a window not unlike the "Find patient" one will open, as regards its features and functions.



Superimposing images

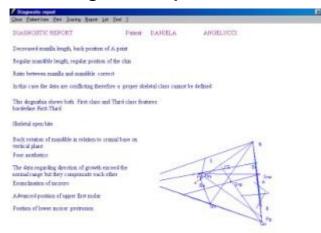
The tracing colour can be defined with the "Select colour" button. Once the first tracing is in position and saved using the "Save first tracing" button, find and select the second tracing, click the "show tracing" button again then double-click with the right button of the mouse to position the second tracing too. To move the tracings around and to superimpose images on any plane, use the buttons located at the top left of the window.

14.0 Report



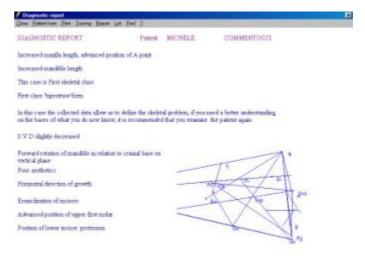
In the "Tracing" window, click "Report" or on the first button from the left on the toolbar and the report (example shown) will be displayed, varying obviously depending on the methodology selected. All programmed values are calculated in line with this choice of methodology and are then compared with normal ranges, sex and age, and a final indication is given of the diagnostic evaluation for each individual value considered without integrating it with all the other values.

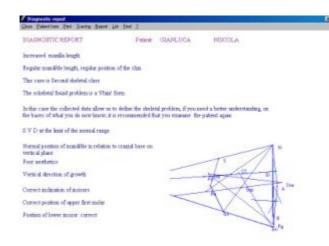
15.0 Diagnostic report



From the report window, click the diagnosis menu or the equivalent button (last one from the right) and LC will integrate the overall values available and will generate as accurate as possible a diagnosis based on the values measured.

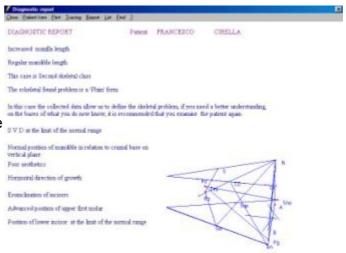
The reliability of the diagnostic report has been tested with over 100 tracings belonging to previously treated patients and it was found to be extremely precise.





Important recommendation: LC generates the diagnostic report based on the assumption that the patient's proportions are not over different from the average person, meaning that for dwarfism or gigantism patients, the reports will not be 100% accurate.

You won't need to be reminded that the final evaluation should be carried out by the patient's doctor, in light of the information he has available (in addition to the cephalometric data), and from which he will be able to identify the clinical significance or otherwise of the values found to be outwith the average ranges.



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LC Classification

LC classifies dysgnathias as follows:

Sagital Relation between maxilla and mandible

>First class

- 1. Simple
- 2. At the limits of the Second class
- 3. At the limits of the Third class
- 4. Biprotruse
- Biretruse

>Second class

- 1. Simple
- 2. Hypo-mandible
- 3. Hypo-maxilla
- 4. Composite

>Third Class

- 1. Simple
- 2. Hyper-mandible
- 3. Hypo-maxilla
- 4. Composite

> Borderline Forms

- 1. First Second
- 2. First Third

>Spurious Forms (Present varying combined elements from both First, Second and Third classes)

- 1. Spurious form verging towards First Class
- 2. Spurious form verging towards Second Class
- 3. Spurious form verging towards Third Class

Skeletal Vertical Dimension

Normal

Borderline

Slightly decreased Slightly increased Skeletal deep bite Skeletal open bite

Direction of Growth

Orthognathic
Compensated
Horizontal
Vertical
Distinct horizontal growth
Distinct vertical growth

16.0 Comparative Analysis Method

Why are there so many types of cepholometric analysis? (there are more than 50!).

It's common knowledge that when the same case is examined using different methods, the results are very often contradictory, why is this?

To calculate the angle between the intersection of two lines, both of which pass through two points (eg. the cranial mandible angle), only one method has been used: the equations of the two lines are calculated, followed by a system of equations, all of which are backed up by the validity of the results! However, orthodontics is not an accurate science, and we are therefore forced to research the same problem with many different methods, often obtaining many different results in the process which are then analysed on the basis of often varying theoretical principles! If there is one "right" answer, what is it?

The comparative analyses method selects a collection of measures from a wide range of cephalometric analyses proposed by various different Authors, each addressing the same problem and in the following order:

- -Sagital relation between maxilla and mandible
- -Skeletal vertical dimension
- -Dento dental and dento basal relationship
- -Aesthetics profile and ratio
- -Growth type

With this system and a fast processing computer, you can easily perform a great number of calculations, compare the relative results and thus reduce the possibility of error.

Just one new measure is introduced in the comparative analyses method: The Class index. This is represented by the ratio between the length of the maxilla (Tmj Sna) and the mandible length (Tmj Pg), the values being obtained from the Harwold tables, and with this ratio it is possible to determine if an eventual discrepancy between the upper and lower base originates in the over or under development of one base rather than the other, regardless of the respective objective values; we can therefore define them as "relative" hypo, hyper or normal mandibles / maxillas.

All in all, the Class index will always give an accurate indication as to whether the bone structure is too small, too big or in proportion compared with the antagonistic bone structure.

Cephalometric analysis has undergone a major advance in the past few decades.

Many advocates enthusiastically poured out an enormous quantity of cephalometric landmarks, some of which were particularly extravagant if not "improbable".

Operating in this sea of opinions means running the risk of perhaps even going off track!

There won't be room for any more landmark points in cephalometrics of the future, the real challenge will be to extrapolate the best possible meaning from the huge number of already existing points.

Lightning Ceph aims to do just this.

17.0 Customised Cephalometric Analyses

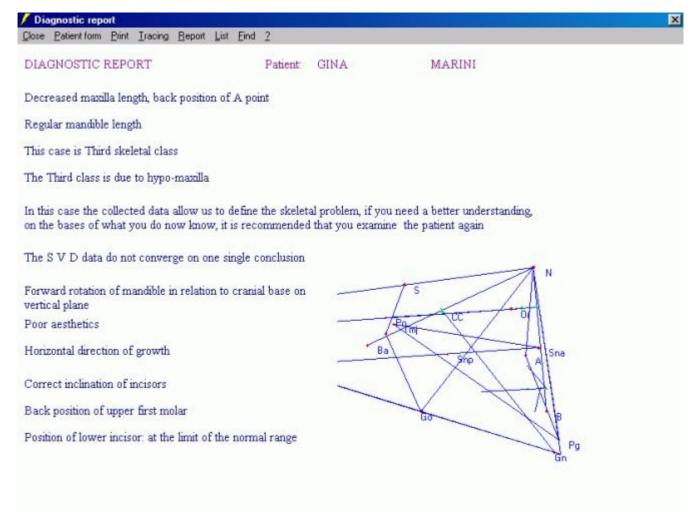


From the patient input form, select "Customised" and the illustrated window will open.

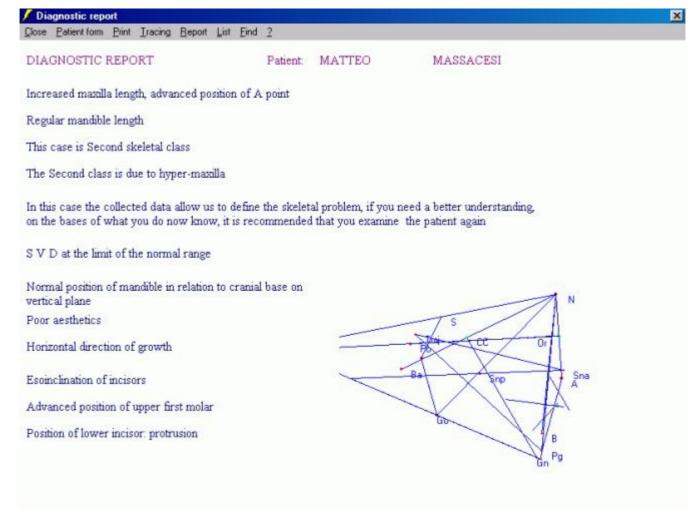
Place an x-ray in front of the screen, or you can equally load-up a previously saved image (either a latero-lateral or postero-anterior projection): if the "Angle" option has been selected, click three times with one of the mouse buttons to locate the three points that define the angle. The first point will be the vertex, the second point defines the first side and the third point the second side. (As is conventionally used, the values are considered as being taken anticlockwise).

To calculate the distance between two points, make the two sides of a triangle coincide, or better still, click the second and third points of the triangle on the same spot with the left then right mouse buttons.

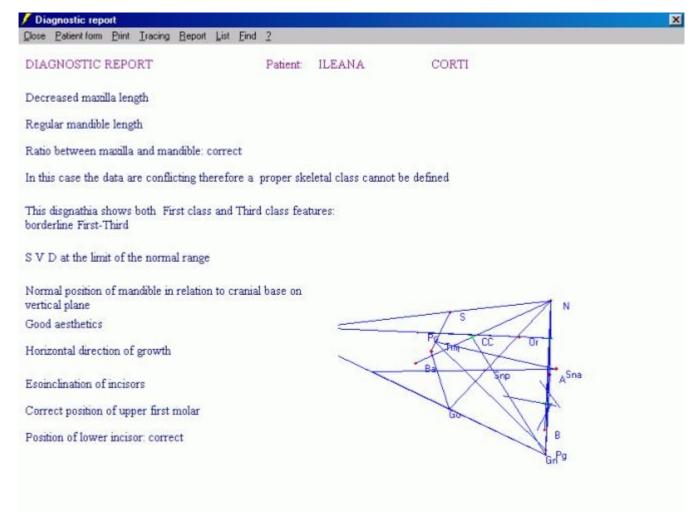
If the "intersection" option has been selected, locate two sets of points that define the two lines for which the intersection point is to be calculated, if the "Projection" option has been selected, the first two points identify the line whilst the third one is the point to be projected through the line.



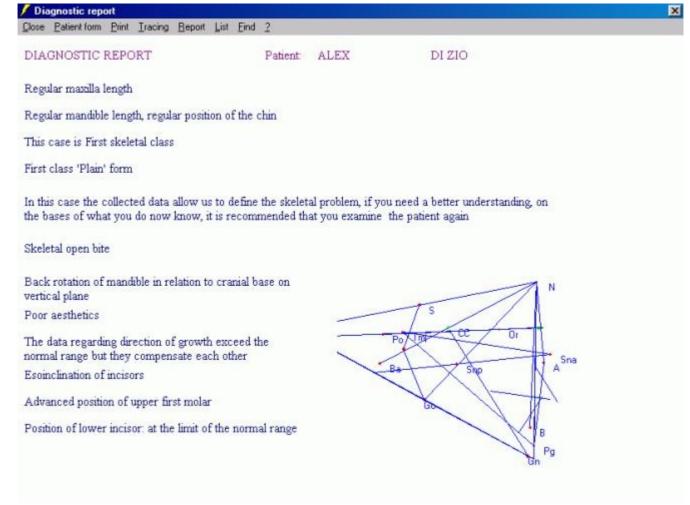
Example 1 Diagnostic Report



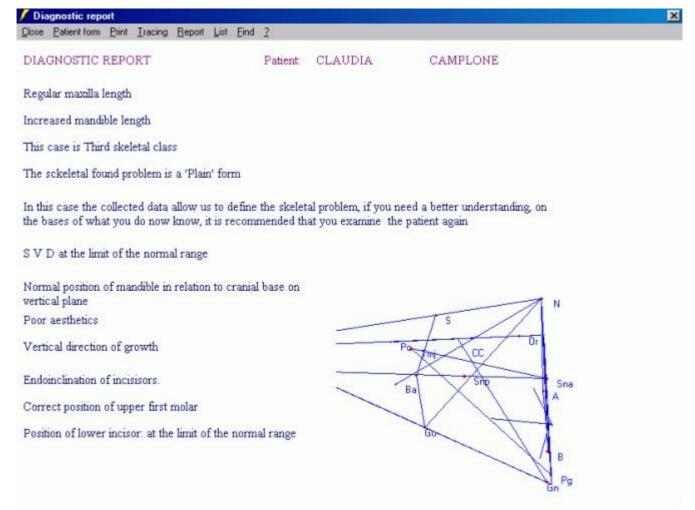
Example 2 Diagnostic Report



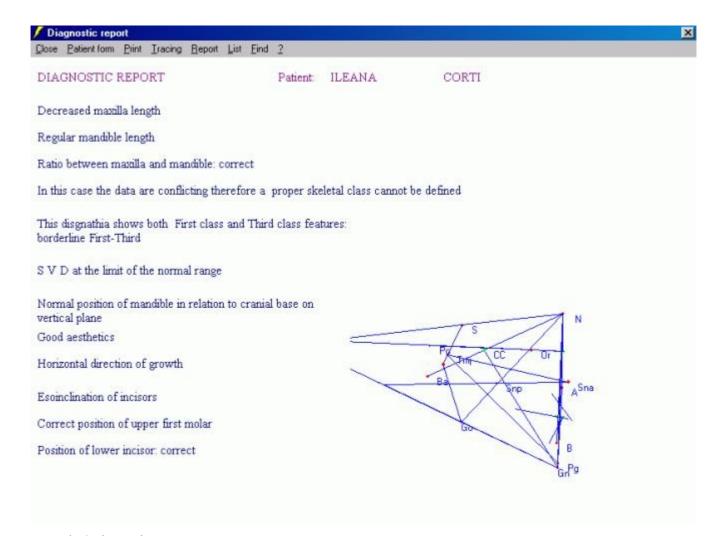
Example 3 diagnostic report



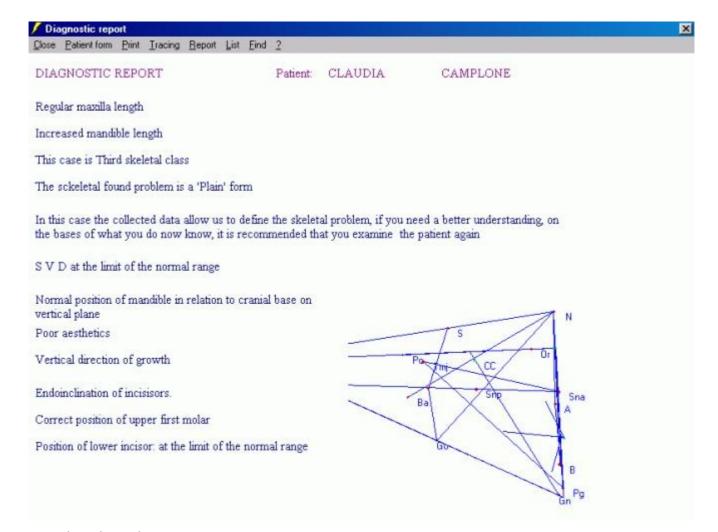
Example 4 diagnostic report



Example 5 diagnostic report



Example 6 Diagnostic Report



Example 7 Diagnostic Report

18.0 ElleSoft s.r.l.

LightningCeph is a software application designed, created and distributed by:

ElleSoft s.r.l.

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http://www.ellesoft.cjb.net/

E-Mail: <u>lightningceph@tin.it</u>

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